

Sequence Listing

(1) GENERAL INFORMATION:

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Chang, Stephen M.W.
Respass, James G.
DePollo, Nicholas J.
Hsu, David Chi-Tang
Ibanez, Carlos E.
Greengard, Judith
Lee, Will

(ii) TITLE OF INVENTION: METHODS FOR ADMINISTRATION OF
RECOMBINANT GENE DELIVERY VEHICLES FOR TREATMENT
OF HEMOPHILIA AND OTHER DISORDERS

(iii) NUMBER OF SEQUENCES: 84

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Seattle
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/001,039
(B) FILING DATE: 13-JAN-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: McMasters, David D.
(B) REGISTRATION NUMBER: 33,963
(C) REFERENCE/DOCKET NUMBER: 1155.005 / 930049.441C4

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
GAGAGATGGG GGAGGCTAAC TGAG

(2) INFORMATION FOR SEQ ID NO:2:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic).
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
GATCCTCAGT TAGCCTCCCC CATCTCTC

(2) INFORMATION FOR SEQ ID NO:3:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
TATATCTCCA GATGAGGTAC ATGATTTTAG GCTTG

(2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
TATATATCGA TTCAAGGCAT TTTCTTTTCA TCAATAAAAC

(2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
TCGAGGATCC GCCCGGGCGG CCGCATCGAT GTCGACG

(2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
CGCGTCGACA TCGATGCGGC CGCCCGGGCG GATCC

24

28

35

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37

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGTGAATTCG AGCTCGGTAC CCGGGGATCC TCTAGAGTCG ACCTGCAGGC ATGCAAGCTT
GGCGTACTCA TGGTCAT

60
77

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Arg Glu Met Gly Glu Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCCGAGAGAT GGGGGAGGCT AACTGAG

27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCTCTCTA CCCCCTCCGA TTGACACCTA G

31

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Ile Met Thr Met
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCTGTGCCT TATTTGAACT AACC

24

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCCACCACAA CCACATATCC CTCC

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCAGTCCTCC GATTGACTG

19

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8332 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGCCAGTCC TCCGATTGAC TGAGTCGCCC GGGTACCCGT GTATCCAATA AACCCCTCTTG

60

CAGTTGCATC CGACTTGTGG TCTCGCTGTT CCTTGGGAGG GTCTCCTCTG AGTGATTGAC

120

TACCCGTCAG CGGGGGTCTT TCATTTGGGG GCTCGTCCGG GATCGGGAGA CCCCTGCCCA

180

GGGACCACCG ACCCACCACC GGGAGGTAAG CTGGCCAGCA ACTTATCTGT GTCTGTCCGA

240

TTGTCTAGTG TCTATGACTG ATTTTATGCG CCTGCGTCGG TACTAGTTAG CTAAGTAGCT

300

CTGTATCTGG CGGACCCGTG GTGGAAGTGA CGAGTTCGGA ACACCCGGCC GCAACCCTGG

360

GAGACGTCCC AGGGACTTCG GGGGCCGTTT TTGTGGCCCG ACCTGAGTCC AAAAATCCCG

420

ATCGTTTTGG ACTCTTTGGT GCACCCCCCT TAGAGGAGGG ATATGTGGTT CTGGTAGGAG	480
ACGAGAACCT AAAACAGTTC CCGCCTCCGT CTGAATTTTT GCTTTCGGTT TGGGACCGAA	540
GCCGCGCCGC GCGTCTTGTC TGCTGCAGCA TCGTTCTGTG TTGTCTCTGT CTGACTGTGT	600
TTCTGTATTT GTCTGAGAAT ATGGGCCAGA CTGTTACCAC TCCCTTAAGT TTGACCTTAG	660
GTCACTGGAA AGATGTCGAG CGGATCGCTC ACAACCAGTC GGTAGATGTC AAGAAGAGAC	720
GTTGGGTTAC CTTCTGCTCT GCAGAATGGC CAACCTTTAA CGTCGGATGG CCGCGAGACG	780
GCACCTTTAA CCGAGACCTC ATCACCAGG TTAAGATCAA GGTCTTTTCA CCTGGCCCGC	840
ATGGACACCC AGACCAGGTC CCTACATCG TGACCTGGGA AGCCTTGGCT TTTGACCCCC	900
CTCCCTGGGT CAAGCCCTTT GTACACCCTA AGCCTCCGCC TCCTCTTCCT CCATCCGCCC	960
CGTCTCTCCC CTTGAACCT CCTCGTTCGA CCCCGCCTCG ATCCTCCCTT TATCCAGCCC	1020
TCACTCCTTC TCTAGGCGCC AAACCTAAAC CTCAAGTTCT TTCTGACAGT GGGGGGCGC	1080
TCATCGACCT ACTTACAGAA GACCCCCCGC CTTATAGGGA CCCAAGACCA CCCCCTTCCG	1140
ACAGGGACGG AAATGGTGGA GAAGCGACGC CTGCGGGAGA GGCACCGGAC CCCTCCCCAA	1200
TGGCATCTCG CCTACGTGGG AGACGGGAGC CCCCTGTGGC CGACTCCACT ACCTCGCAGG	1260
CATTCCCCCT CCGCGCAGGA GGAAACGGAC AGCTTCAATA CTGGCCGTTT TCCTCTTCTG	1320
ACCTTTACAA CTGGAAAAAT AATAACCCTT CTTTTTCTGA AGATCCAGGT AACTGACAG	1380
CTCTGATCGA GTCTGTTCTC ATCACCATC AGCCACCTG GGACGACTGT CAGCAGCTGT	1440
TGGGGACTCT GCTGACCGGA GAAGAAAAAC AACGGGTGCT CTTAGAGGCT AGAAAGGCGG	1500
TGCGGGGCGA TGATGGGCGC CCCACTCAAC TGCCCAATGA AGTCGATGCC GCTTTTCCCC	1560
TCGAGCGCCC AGACTGGGAT TACACCACCC AGGCAGGTAG GAACCACCTA GTCCACTATC	1620
GCCAGTTGCT CTTAGCGGGT CTCCAAAACG CGGGCAGAAG CCCACCAAT TTGGCCAAGG	1680
TAAAAGGAAT AACACAAGGG CCCAATGAGT CTCCCTCGGC CTTCTTAGAG AGACTTAAGG	1740
AAGCCTATCG CAGGTACACT CTTATGACC CTGAGGACCC AGGGCAAGAA ACTAATGTGT	1800
CTATGTCTTT CATTTGGCAG TCTGCCCCAG ACATTGGGAG AAAGTTAGAG AGGTTAGAAG	1860
ATTTAAAAAA CAAGACGCTT GGAGATTTGG TTAGAGAGGC AGAAAAGATC TTTAATAAAC	1920
GAGAAACCCC GGAAGAAAGA GAGGAACGTA TCAGGAGAGA AACAGAGGAA AAAGAAGAAC	1980
GCCGTAGGAC AGAGGATGAG CAGAAAGAGA AAGAAAGAGA TCGTAGGAGA CATAGAGAGA	2040

TGAGCAAGCT ATTGGCCACT GTCGTTAGTG GACAGAAACA GGATAGACAG GGAGGAGAAC	2100
GAAGGAGGTC CCAACTCGAT CGCGACCACT GTGCCTACTG CAAAGAAAAG GGGCACTGGG	2160
CTAAAGATTG TCCCAAGAAA CCACGAGGAC CTCGGGGACC AAGACCCAG ACCTCCCTCC	2220
TGACCCTAGA TGA TAGGGA GGTCAGGGTC AGGAGCCCCC CCCTGAACCC AGGATAACCC	2280
TCAAAGTCGG GGGGCAACCC GTCACCTTCC TGGTAGATAC TGGGGCCCAA CACTCCGTGC	2340
TGACCCAAAA TCCTGGACCC CTAAGTGATA AGTCTGCCTG GGTCCAAGGG GCTACTGGAG	2400
GAAAGCGGTA TCGCTGGACC ACGGATCGCA AAGTACATCT AGCTACCGGT AAGGTCACCC	2460
ACTCTTTCCT CCATGTACCA GACTGTCCCT ATCCTCTGTT AGGAAGAGAT TTGCTGACTA	2520
AACTAAAAGC CCAAATCCAC TTTGAGGGAT CAGGAGCTCA GGTATATGGGA CCAATGGGGC	2580
AGCCCCTGCA AGTGTTGACC CTAAATATAG AAGATGAGCA TCGGCTACAT GAGACCTCAA	2640
AAGAGCCAGA TGTTTCTCTA GGGTCCACAT GGCTGTCTGA TTTTCTCAG GCCTGGGCGG	2700
AAACCGGGGG CATGGGACTG GCAGTTCGCC AAGCTCCTCT GATCATACT CTGAAAGCAA	2760
CCTCTACCCC CGTGTCCATA AAACAATACC CCATGTCACA AGAAGCCAGA CTGGGGATCA	2820
AGCCCCACAT ACAGAGACTG TTGGACCAGG GAATACTGGT ACCCTGCCAG TCCCCCTGGA	2880
ACACGCCCCCT GCTACCCGTT AAGAAACCAG GGACTAATGA TTATAGGCCT GTCCAGGATC	2940
TGAGAGAAGT CAACAAGCGG GTGGAAGACA TCCACCCAC CGTGCCCAAC CCTTACAACC	3000
TCTTGAGCGG GCTCCCACCG TCCCACCAGT GGTACACTGT GCTTGATTTA AAGGATGCCT	3060
TTTTCTGCCT GAGACTCCAC CCCACCAGTC AGCCTCTCTT CGCCTTTGAG TGGAGAGATC	3120
CAGAGATGGG AATCTCAGGA CAATTGACCT GGACCAGACT CCCACAGGGT TTCAAAAACA	3180
GTCCCACCCT GTTTGATGAG GCACTGCACA GAGACCTAGC AGACTTCCGG ATCCAGCACC	3240
CAGACTTGAT CTGCTACAG TACGTGGATG ACTTACTGCT GGCCGCCACT TCTGAGCTAG	3300
ACTGCCAACA AGGTACTCGG GCCCTGTTAC AAACCCTAGG GAACCTCGGG TATCGGGCCT	3360
CGGCCAAGAA AGCCCAAATT TGCCAGAAAC AGGTCAAGTA TCTGGGGTAT CTTCTAAAAG	3420
AGGGTCAGAG ATGGCTGACT GAGGCCAGAA AAGAGACTGT GATGGGGCAG CCTACTCCGA	3480
AGACCCCTCG ACAACTAAGG GAGTTCCTAG GGACGGCAGG CTTCTGTGCG CTCTGGATCC	3540
CTGGGTTTGC AGAAATGGCA GCCCCCTTGT ACCCTCTCAC CAAAACGGGG ACTCTGTTTA	3600
ATTGGGGCCC AGACCAACAA AAGGCCTATC AAGAAATCAA GCAAGCTCTT CTAAGTCCCC	3660

CAGCCCTGGG GTTGCCAGAT TTGACTAAGC CCTTTGAACT CTTTGTGAC GAGAAGCAGG	3720
GCTACGCCAA AGGTGTCCTA ACGCAAAAAC TGGGACCTTG GCGTCGGCCG GTGGCCTACC	3780
TGTCCAAAAA GCTAGACCCA GTAGCAGCTG GGTGGCCCCC TTGCCTACGG ATGGTAGCAG	3840
CCATTGCCGT ACTGACAAAG GATGCAGGCA AGCTAACCAT GGGACAGCCA CTAGTCATTC	3900
TGGCCCCCA TGCAGTAGAG GCACTAGTCA AACAACCCCC CGACCGCTGG CTTTCCAACG	3960
CCCGGATGAC TCACTATCAG GCCTTGCTTT TGGACACGGA CCGGGTCCAG TTCGGACCGG	4020
TGGTAGCCCT GAACCCGGCT ACGCTGCTCC CACTGCCTGA GGAAGGGCTG CAACACAAC	4080
GCCTTGATAT CCTGGCCGAA GCCCACGGAA CCGACCCGA CCTAACGGAC CAGCCGCTCC	4140
CAGACGCCGA CCACACCTGG TACACGGATG GAAGCAGTCT CTTACAAGAG GGACAGCGTA	4200
AGGCGGGAGC TCGGTGACC ACCGAGACCG AGGTAATCTG GGCTAAAGCC CTGCCAGCCG	4260
GGACATCCGC TCAGCGGGCT GAACTGATAG CACTCACCCA GGCCCTAAAG ATGGCAGAAG	4320
GTAAGAAGCT AAATGTTTAT ACTGATAGCC GTTATGCTTT TGCTACTGCC CATATCCATG	4380
GAGAAATATA CAGAAGGCGT GGGTTGCTCA CATCAGAAGG CAAAGAGATC AAAAATAAAG	4440
ACGAGATCTT GGCCCTACTA AAAGCCCTCT TTCTGCCCAA AAGACTTAGC ATAATCCATT	4500
GTCCAGGACA TCAAAGGGA CACAGCGCCG AGGCTAGAGG CAACCGGATG GCTGACCAAG	4560
CGGCCCGAAA GGCAGCCATC ACAGAGACTC CAGACACCTC TACCCTCCTC ATAGAAAATT	4620
CATCACCTA CACCTCAGAA CATTTCATT ACACAGTGAC TGATATAAAG GACCTAACCA	4680
AGTTGGGGGC CATTTATGAT AAAACAAAGA AGTATTGGGT CTACCAAGGA AACCTGTGA	4740
TGCCTGACCA GTTTACTTTT GAATTATTAG ACTTCTTCA TCAGCTGACT CACCTCAGCT	4800
TCTCAAAAAT GAAGGCTCTC CTAGAGAGAA GCCACAGTCC CTACTACATG CTGAACCGGG	4860
ATCGAACACT CAAAATATC ACTGAGACCT GCAAAGCTTG TGCACAAGTC AACGCCAGCA	4920
AGTCTGCCGT TAAACAGGGA ACTAGGGTCC GCGGGCATCG GCCCGGCACT CATTGGGAGA	4980
TCGATTTCAC CGAGATAAAG CCCGGATTGT ATGGCTATAA ATATCTTCTA GTTTTATAG	5040
ATACCTTTTC TGGCTGGATA GAAGCCTTCC CAACCAAGAA AGAAACCGCC AAGGTCGTAA	5100
CCAAGAAGCT ACTAGAGGAG ATCTTCCCCA GGTTCCGGCAT GCCTCAGGTA TTGGGAACTG	5160
ACAATGGGCC TGCCTTCGTC TCCAAGGTGA GTCAGACAGT GGCCGATCTG TTGGGGATTG	5220
ATTGGAAATT ACATTGTGCA TACAGACCCC AAAGCTCAGG CCAGGTAGAA AGAATGAATA	5280

GAACCATCAA GGAGACTTTA ACTAAATTAA CGCTTGCAAC TGGCTCTAGA GACTGGGTGC	5340
TCCTACTCCC CTTAGCCCTG TACCGAGCCC GCAACACGCC GGGCCCCCAT GGCTTCACCC	5400
CATATGAGAT CTTATATGGG GCACCCCCGC CCCTTGTAAG CTTCCCTGAC CCTGACATGA	5460
CAAGAGTTAC TAACAGCCCC TCTCTCCAAG CTCACTTACA GGCTCTCTAC TTAGTCCAGC	5520
ACGAAGTCTG GAGACCTCTG GCGGCAGCCT ACCAAGAACA ACTGGACCGA CCGGTGGTAC	5580
CTCACCCTTA CCGAGTCGGC GACACAGTGT GGGTCCGCCG ACACCAGACT AAGAACCTAG	5640
AACCTCGCTG GAAAGGACCT TACACAGTCC TGCTGACCAC CCCCACCGCC CTCAAAGTAG	5700
ACGGCATCGC AGCTTGATA CACGCCGCC ACGTGAAGGC TGCCGACCCC GGGGGTGGAC	5760
CATCCTCTAG ACTGACATGG CGCGTTCAAC GCTCTCAAAA CCCCTTAAAA ATAAGGTAA	5820
CCCGCGAGGC CCCCTAATCC CCTTAATTCT TCTGATGCTC AGAGGGGTCA GTACTGCTTC	5880
GCCCGGCTCC AGTCCTCATC AAGTCTATAA TATCACCTGG GAGGTAACCA ATGGAGATCG	5940
GGAGACGGTA TGGGCAACTT CTGGCAACCA CCCTCTGTGG ACCTGGTGGC CTGACCTTAC	6000
CCCAGATTTA TGTATGTTAG CCCACCATGG ACCATCTTAT TGGGGGCTAG AATATCAATC	6060
CCCTTTTCT TCTCCCCCGG GGCCCCCTTG TTGCTCAGGG GGCAGCAGCC CAGGCTGTTC	6120
CAGAGACTGC GAAGAACCTT TAACCTCCCT CACCCCTCGG TGCAACACTG CCTGGAACAG	6180
ACTCAAGCTA GACCAGACAA CTCATAAATC AAATGAGGGA TTTTATGTTT GCCCCGGGCC	6240
CCACCGCCCC CGAGAATCCA AGTCATGTGG GGGTCCAGAC TCCTTCTACT GTGCCTATTG	6300
GGGCTGTGAG ACAACCGGTA GAGCTTACTG GAAGCCCTCC TCATCATGGG ATTTTCATCAC	6360
AGTAAACAAC AATCTCACCT CTGACCAGGC TGTCCAGGTA TGCAAAGATA ATAAGTGGTG	6420
CAACCCCTTA GTTATTCGGT TTACAGACGC CGGGAGACGG GTTACTTCCT GGACCACAGG	6480
ACATTACTGG GGCTTACGTT TGTATGTCTC CGGACAAGAT CCAGGGCTTA CATTTGGGAT	6540
CCGACTCAGA TACCAAATC TAGGACCCCG CGTCCCAATA GGGCCAAACC CCGTTCTGGC	6600
AGACCAACAG CCACTCTCCA AGCCCAAACC TGTTAAGTCG CTTTCAGTCA CCAAACCACC	6660
CAGTGGGACT CCTCTCTCCC CTACCCAACT TCCACCGGCG GGAACGGAAA ATAGGCTGCT	6720
AACTTAGTA GACGGAGCCT ACCAAGCCCT CAACCTCACC AGTCCTGACA AAACCAAGA	6780
GTGCTGGTTG TGTCTAGTAG CGGGACCCCC CTACTACGAA GGGGTGCGG TCCTGGGTAC	6840
CTACTCCAAC CATACTCTG CTCCAGCCAA CTGCTCCGTG GCCTCCCAAC ACAAGTTGAC	6900

CCTGTCCGAA GTGACCGGAC AGGGACTCTG CATAGGAGCA GTTCCCAAAA CACATCAGGC	6960
CCTATGTAAT ACCACCCAGA CAAGCAGTCG AGGGTCCTAT TATCTAGTTG CCCCTACAGG	7020
TACCATGTGG GCTTGTAAGTA CCGGGCTTAC TCCATGCATC TCCACCACCA TACTGAACCT	7080
TACCACTGAT TATTGTGTTT TTGTCGAACT CTGGCCAAGA GTCACCTATC ATTCCCCCAG	7140
CTATGTTTAC GGCCTGTTTG AGAGATCCAA CCGACACAAA AGAGAACCGG TGTCGTTAAC	7200
CCTGGCCCTA TTATTGGGTG GACTAACCAT GGGGGGAATT GCCGCTGGAA TAGGAACAGG	7260
GACTACTGCT CTAATGGCCA CTCAGCAATT CCAGCAGCTC CAAGCCGCAG TACAGGATGA	7320
TCTCAGGGAG GTTGAAAAAT CAATCTCTAA CCTAGAAAAG TCTCTCACTT CCCTGTCTGA	7380
AGTTGTCTTA CAGAATCGAA GGGGCCTAGA CTTGTTATTT CTAAAAGAAG GAGGGCTGTG	7440
TGCTGCTCTA AAAGAAGAAT GTTGCTTCTA TCGGACCAC ACAGGACTAG TGAGAGACAG	7500
CATGGCCAAA TTGAGAGAGA GGCTTAATCA GAGACAGAAA CTGTTTGAGT CAACTCAAGG	7560
ATGGTTTGAG GGACTGTTTA ACAGATCCCC TTGGTTTACC ACCTTGATAT CTACCATTAT	7620
GGGACCCCTC ATTGTACTCC TAATGATTTT GCTCTTCGGA CCCTGCATTC TTAATCGATT	7680
AGTCCAATTT GTTAAAGACA GGATATCAGT GGTCCAGGCT CTAGTTTGA CTCAACAATA	7740
TCACCAGCTG AAGCCTATAG AGTACGAGCC ATAGATAAAA TAAAGATTT TATTTAGTCT	7800
CCAGAAAAAG GGGGGAATGA AAGACCCAC CTGTAGGTTT GGCAAGCTAG CTTAAGTAAC	7860
GCCATTTTGC AAGGCATGGA AAAATACATA ACTGAGAATA GAGAAGTTCA GATCAAGGTC	7920
AGGAACAGAT GGAACAGCTG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG	7980
CCCCGGCTCA GGGCCAAGAA CAGATGGAAC AGCTGAATAT GGGCCAAACA GGATATCTGT	8040
GGTAAGCAGT TCCTGCCCCG GCTCAGGGCC AAGAACAGAT GGTCCCCAGA TCGGTCCAG	8100
CCCTCAGCAG TTTCTAGAGA ACCATCAGAT GTTCCAGGG TGCCCCAAGG ACCTGAAATG	8160
ACCCTGTGCC TTATTTGAAC TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC	8220
TGCTCCCCGA GCTCAATAAA AGAGCCACA ACCCCTCACT CGGGGCGCCA GTCCTCCGAT	8280
TGACTGAGTC GCCCGGGTAC CCGTGTATCC AATAAACCTT CTTGCAGTTG CA	8332

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
GGGAGTGGTA ACAGTCTGGC CTTAATTCTC AG

(2) INFORMATION FOR SEQ ID NO:17:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:
CGGTGACCT CGAGAATTAA TTC

(2) INFORMATION FOR SEQ ID NO:18:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:
CTGGGAGACG TCCCAGGGAC TTC

(2) INFORMATION FOR SEQ ID NO:19:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:
GGCCAGACTG TTACCACTCC CTGAAGTTTG AC

(2) INFORMATION FOR SEQ ID NO:20:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:
CATCGATAAA ATAAAAGATT TTATTAGTC

(2) INFORMATION FOR SEQ ID NO:21:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:
CAAATGAAAG ACCCCGCTG AC

32

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(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
GAAGCTTCTC CCAGAACCCA CCAGTCTTGA AACGCCATC

39

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
GTACCAGCTT TTGGTCTCAT CAAAG

25

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:
CTCCTCGAGC TAAAGATATT TTAGAGAAGA ATTAAC

36

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:
TTCCTCTGGA CAGCTGTCTA CTTTG

25

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
TCGAGGGGCC CAGATCTGCG GCCGCTCGCG AGTCGACAAG CTTGGATCCA T

51

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:
CGATGGATCC AAGCTTGTCG ACTCGCGAGC GGCCGCAGAT CTGGGCCCC

49

(2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
CACCGTCGTC GACTTATGCT

20

(2) INFORMATION FOR SEQ ID NO:29:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
GACCGTCGAC TCAATTCTGG GAGAAGCTTC TTGG

34

(2) INFORMATION FOR SEQ ID NO:30:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
CACCGTCGTC GACTTATGCT

20

(2) INFORMATION FOR SEQ ID NO:31:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
CAACGCTCGA GAAGCAGAAT CGCAAAAGGC

30

(2) INFORMATION FOR SEQ ID NO:32:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
TCGGCTCGAG GCATCAACGG GAAATAACTC GT

32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
CCGACTCGAG TCAGTAGAGG TCCTGTGCCT C

31

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
GCGACTCGAG CATGGGGCCC TGGGGC

26

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
GCACTGGAAT TCGTCAGGGC G

21

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
CGCGCCGCTC GAGTCTACAA TGGCCTTGAC CTTTGCTTTA CTGG

44

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
GCGCCCATCG ATTCAATCCT TACTTCTTAA ACTTTCTTGC AAG

43

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGCGCCGCTC GAGCATCCAA TGGCCCTGTC CTTTCTTTA CTTATGG

47

(2) INFORMATION FOR SEQ-ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCATCGATTG AATCCTTCCT CCTTAATCTT TTTTGCAAG

39

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCGGATCCTC TACAATGGCC TTGACCTTG CTTTACTGG

39

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGCGCCGGCG GCCGCTCATT CTTACTTCT TAACTTTCT TGCAAG

46

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CCGGATCCCA TCCAATGGCC CTGTCCTTTT CTTTACTTAT GG

42

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:
 CGCGCCGGCG GCCGCTCAAT CCTTCCTCCT TAATCTTTTT TGCAAG

46

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GGGGGGGGGG	GGGGGGGGGG	GGGTGAGCAC	ATCCAGTGGG	TAAAGTTCCT	TAAAATGCTC	60
TGCAAAGAAA	TTGGGACTTT	TCATTAAATC	AGAAATTTTA	CTTTTTTCCC	CTCCTGGGAG	120
CTAAAGATAT	TTTAGAGAAG	AATTAACCTT	TTGCTTCTCC	AGTTGAACAT	TTGTAGCAAT	180
AAGTCATGCA	AATAGAGCTC	TCCACCTGCT	TCTTTCTGTG	CCTTTTGCGA	TTCTGCTTTA	240
GTGCCACCAG	AAGATACTAC	CTGGGTGCAG	TGGAAGTGTG	ATGGGACTAT	ATGCAAAGTG	300
ATCTCGGTGA	GCTGCCTGTG	GACGCAAGAT	TTCCTCCTAG	AGTGCCAAAA	TCTTTTCCAT	360
TCAACACCTC	AGTCGTGTAC	AAAAAGACTC	TGTTTGTAGA	ATTCACGGAT	CACCTTTTCA	420
ACATCGCTAA	GCCAAGGCCA	CCCTGGATGG	GTCTGCTAGG	TCCTACCATC	CAGGCTGAGG	480
TTTATGATAC	AGTGGTCAAT	ACACTTAAGA	ACATGGCTTC	CCATCCTGTC	AGTCTTCATG	540
CTGTTGGTGT	ATCCTACTGG	AAAGCTTCTG	AGGGAGCTGA	ATATGATGAT	CAGACCAGTC	600
AAAGGGAGAA	AGAAGATGAT	AAAGTCTTCC	CTGGTGGAAG	CCATACATAT	GTCTGGCAGG	660
TCCTGAAAGA	GAATGGTCCA	ATGGCCTCTG	ACCCACTGTG	CCTTACCTAC	TCATATCTTT	720
CTCATGTGGA	CCTGGTAAAA	GACTTGAATT	CAGGCCTCAT	TGGAGCCCTA	CTAGTATGTA	780
GAGAAGGGAG	TCTGGCCAAG	GAAAAGACAC	AGACCTTGCA	CAAATTTATA	CTACTTTTGT	840
CTGTATTTGA	TGAAGGGAAA	AGTTGGCACT	CAGAAACAAA	GAATCCTTG	ATGCAGGATA	900
GGGATGCTGC	ATCTGCTCGG	GCCTGGCCTA	AAATGCACAC	AGTCAATGGT	TATGTAAACA	960
GGTCTCTGCC	AGGTCTGATT	GGATGCCACA	GGAAATCAGT	CTATTGGCAT	GTGATTGGAA	1020
TGGGCACCAC	TCCTGAAGTG	CACTCAATAT	TCCTCGAAGG	TCACACATTT	CTTGTGAGGA	1080
ACCATCGCCA	GGCGTCCTTG	GAAATCTCGC	CAATAACTTT	CCTTACTGCT	CAAACACTCT	1140
TGATGGACCT	TGGACAGTTT	CTACTGTTTT	GTCATATCTC	TTCCCACCAA	CATGATGGCA	1200
TGGAAGCTTA	TGTCAAAGTA	GACAGCTGTC	CAGAGGAACC	CCAACCTACG	ATGAAAAATA	1260
ATGAAGAAGC	GGAAGACTAT	GATGATGATC	TTACTGATTC	TGAAATGGAT	GTGGTCAGGT	1320
TTGATGATGA	CAACTCTCCT	TCCTTTATCC	AAATTCGCTC	AGTTGCCAAG	AAGCATCCTA	1380
AACTTTGGGT	ACATTACATT	GCTGCTGAAG	AGGAGGACTG	GGACTATGCT	CCCTTAGTCC	1440
TCGCCCCCGA	TGACAGAAGT	TATAAAAGTC	AATATTTGAA	CAATGGCCCT	CAGCGGATTG	1500
GTAGGAAGTA	CAAAAAAGTC	CGATTTATGG	CATACACAGA	TGAAACCTTT	AAGACTCGTG	1560
AAGCTATTCA	GCATGAATCA	GGAATCTTGG	GACCTTTACT	TTATGGGGAA	GTTGGAGACA	1620
CACTGTTGAT	TATATTTAAG	AATCAAGCAA	GCAGACCATA	TAACATCTAC	CCTCACGGAA	1680
TCACTGATGT	CCGTCCTTTG	TATTCAAGGA	GATTACCAA	AGGTGTAAAA	CATTTGAAGG	1740
ATTTTCCAAT	TCTGCCAGGA	GAAATATTCA	AATATAAATG	GACAGTGACT	GTAGAAGATG	1800
GGCCAACTAA	ATCAGATCCT	CGGTGCCTGA	CCCGCTATTA	CTCTAGTTTC	GTTAATATGG	1860
AGAGAGATCT	AGCTTCAGGA	CTCATTGGCC	CTCTCCTCAT	CTGCTACAAA	GAATCTGTAG	1920
ATCAAAGAGG	AAACCAGATA	ATGTCAGACA	AGAGGAATGT	CATCCTGTTT	TCTGTATTTG	1980
ATGAGAACCG	AAGCTGGTAC	CTCACAGAGA	ATATACAACG	CTTTCTCCCC	AATCCAGCTG	2040
GAGTGCAGCT	TGAGGATCCA	GAGTTCCAAG	CCTCCAACAT	CATGCACAGC	ATCAATGGCT	2100
ATGTTTTTGA	TAGTTTGCAG	TTGTCAGTTT	GTTTGCATGA	GGTGGCATA	TGGTACATTC	2160
TAAGCATTGG	AGCACAGACT	GACTTCCTTT	CTGTCTTCTT	CTCTGGATAT	ACCTTCAAAC	2220
ACAAAATGGT	CTATGAAGAC	AACTCACCC	TATTCCCAT	CTCAGGAGAA	ACTGTCTTCA	2280

TGTCGATGGA	AAACCCAGGT	CTATGGATTG	TGGGGTGCCA	CAACTCAGAC	TTTCGGAACA	2340
GAGGCATGAC	CGCCTTACTG	AAGGTTTCTA	GTTGTGACAA	GAACACTGGT	GATTATTACG	2400
AGGACAGTTA	TGAAGATATT	TCAGCATACT	TGCTGAGTAA	AAACAATGCC	ATTGAACCAA	2450
GAAGCTTCTC	CCAGAATTCA	AGACACCCTA	GCACTAGGCA	AAAGCAATTT	AATGCCACCA	2520
CAATTCAGGA	AAATGACATA	GAGAAGACTG	ACCCTTGTTT	TGCACACAGA	ACACCTATGC	2580
CTAAAATACA	AAATGTCTCC	TCTAGTGATT	TGTTGATGCT	CTTGCGACAG	AGTCCTACTC	2640
CACATGGGCT	ATCCTTATCT	GATCTCCAAG	AAGCCAAATA	TGAGACTTTT	TCTGATGATC	2700
CATCACCTGG	AGCAATAGAC	AGTAATAACA	GCCTGTCTGA	AATGACACAC	TTCAGGCCAC	2750
AGCTCCATCA	CAGTGGGGAC	ATGGTATTTA	CCCCTGAGTC	AGGCCTCCAA	TTAAGATTAA	2820
ATGAGAAACT	GGGGACAAC	GCAGCAACAG	AGTTGAAGAA	ACTTGATTTT	AAAGTTTCTA	2880
GTACATCAAA	TAATCTGATT	TCAACAATTC	CATCAGACAA	TTTGGCAGCA	GGTACTGATA	2940
ATACAAGTTC	CTTAGGACCC	CCAAGTATGC	CAGTTCATTA	TGATAGTCAA	TTAGATACCA	3000
CTCTATTTGG	CAAAAAGTCA	TETCCCCCTA	CTGAGTCTGG	TGGACCTCTG	AGCTTGAGTG	3060
AAGAAAATAA	TGATTCAAAG	TTGTTAGAAT	CAGGTTTAA	GAATAGCCAA	GAAAGTTCAT	3120
GGGGAAAAAA	TGTATCGTCA	ACAGAGAGTG	GTAGGTTATT	TAAAGGGAAA	AGAGCTCATG	3180
GACCTGCTTT	GTTGACTAAA	GATAATGCCT	TATTCAAAGT	TAGCATCTCT	TTGTTAAAGA	3240
CAAACAAAAC	TTCCAATAAT	TCAGCAACTA	ATAGAAAGAC	TCACATTGAT	GGCCCATCAT	3300
TATTAATTGA	GAATAGTCCA	TCAGTCTGGC	AAAATATATT	AGAAAGTGAC	ACTGAGTTTA	3360
AAAAAGTGAC	ACCTTTGATT	CATGACAGAA	TGCTTATGGA	CAAAAATGCT	ACAGCTTTGA	3420
GGCTAAATCA	TATGTCAAAT	AAAACACTTT	CATCAAAAAA	CATGGAAATG	GTCCAACAGA	3480
AAAAAGAGGG	CCCCATTCCA	CCAGATGCAC	AAAATCCAGA	TATGTCGTTT	TTTAAGATGC	3540
TATTCCTTGGC	AGAATCAGCA	AGGTGGATAC	AAAGGACTCA	TGGAAAGAAC	TCTCTGAACT	3600
CTGGGCAAGG	CCCCAGTCCA	AAGCAATTAG	TATCCTTAGG	ACCAGAAAAA	TCTGTGGAAG	3660
GTCAGAATTT	CTTGTCTGAG	AAAAACAAAG	TGGTAGTAGG	AAAGGGTGAA	TTTACAAAGG	3720
ACGTAGGACT	CAAAGAGATG	GTTTTTCCAA	GCAGCAGAAA	CCTATTTCTT	ACTAACTTGG	3780
ATAATTTACA	TGAAAATAAT	ACACACAATC	AAGAAAAAAA	AATTCAGGAA	GAAATAGAAA	3840
AGAAGGAAAC	ATTAATCCAA	GAGAATGTAG	TTTTGCCTCA	GATACATACA	GTGACTGGCA	3900
CTAAGAATTT	CATGAAGAAC	CTTTTCTTAC	TGAGCACTAG	GCAAAATGTA	GAAGGTTTCAT	3960
ATGACGGGGC	ATATGCTCCA	GTACTTCAAG	ATTTTAGGTC	ATTAAATGAT	TCAACAAATA	4020
GAACAAAGAA	ACACACAGCT	CATTTCTCAA	AAAAAGGGGA	GGAAGAAAAC	TTGGAAGGCT	4080
TGGGAAATCA	AACCAAGCAA	ATTGTAGAGA	AATATGCATG	CACCACAAGG	ATATCTCCTA	4140
ATACAAGCCA	GCAGAATTTT	GTCACGCAAC	GTAATAAGAG	AGCTTTGAAA	CAATTCAGAC	4200
TCCCACCTAGA	AGAAACAGAA	CTTGAAAAAA	GGATAATTGT	GGATGACACC	TCAACCCAGT	4260
GGTCCAAAAA	CATGAAACAT	TTGACCCCGA	GCACCCTCAC	ACAGATAGAC	TACAATGAGA	4320
AGGAGAAAGG	GGCCATTACT	CAGTCTCCCT	TATCAGATTG	CCTTACGAGG	AGTCATAGCA	4380
TCCCTCAAGC	AAATAGATCT	CCATTACCCA	TTGCAAAGGT	ATCATCATTT	CCATCTATTA	4440
GACCTATATA	TCTGACCAGG	GTCCTATTCC	AAGACAACCT	TTCTCATCTT	CCAGCAGCAT	4500
CTTATAGAAA	GAAAGATTCT	GGGGTCCAAG	AAAGCAGTCA	TTTCTTACAA	GGAGCCAAAA	4560
AAAATAACCT	TTCTTTAGCC	ATTCTAACCT	TGGAGATGAC	TGGTGATCAA	AGAGAGGTTG	4620
GCTCCCTGGG	GACAAGTGCC	ACAAATTCAG	TCACATACAA	GAAAGTTGAG	AACACTGTTC	4680
TCCCGAAACC	AGACTTGCCC	AAAACATCTG	GCAAAGTTGA	ATTGCTTCCA	AAAGTTCACA	4740
TTTATCAGAA	GGACCTATTG	CCTACGGAAA	CTAGCAATGG	GTCTCCTGGC	CATCTGGATC	4800
TCGTGGAAGG	GAGCCTTCTT	CAGGGAACAG	AGGGAGCGAT	TAAGTGGAA	GAAGCAAACA	4860
GACCTGGAAA	AGTTCCCTTT	CTGAGAGTAG	CAACAGAAAG	CTCTGCAAAG	ACTCCCTCCA	4920
AGCTATTGGA	TCCTCTTGCT	TGGGATAACC	ACTATGGTAC	TCAGATACCA	AAAGAAGAGT	4980
GGAAATCCCA	AGAGAAGTCA	CCAGAAAAAA	CAGCTTTTAA	GAAAAAGGAT	ACCATTTTGT	5040
CCCTGAACGC	TTGTGAAAGC	AATCATGCAA	TAGCAGCAAT	AAATGAGGGA	CAAAATAAGC	5100
CCGAAATAGA	AGTCACCTGG	GCAAAGCAAG	GTAGGACTGA	AAGGCTGTGC	TCTCAAAACC	5160
CACCAGTCTT	GAAACGCCAT	CAACGGGAAA	TAACCTCGTAC	TACTCTTCAG	TCAGATCAAG	5220
AGGAAATTGA	CTATGATGAT	ACCATATCAG	TTGAAATGAA	GAAGGAAGAT	TTTGACATTT	5280
ATGATGAGGA	TGAAAATCAG	AGCCCCCGCA	GCTTTTCAAAA	GAAAACACGA	CACTATTTTA	5340
TTGCTGCAGT	GGAGAGGCTC	TGGGATTATG	GGATGAGTAG	CTCCCCACAT	GTTCTAAGAA	5400
ACAGGGCTCA	GAGTGGCAGT	GTCCCTCAGT	TCAAGAAAGT	TGTTTTCCAG	GAATTTACTG	5460
ATGGCTCCTT	TACTCAGCCC	TTATACCGTG	GAGAACTAAA	TGAACATTTG	GGACTCCTGG	5520

GGCCATATAT	AAGAGCAGAA	GTTGAAGATA	ATATCATGGT	AACTTTCAGA	AATCAGGCCT	5580
CTCGTCCCTA	TTCCTTCTAT	TCTAGCCTTA	TTTCTTATGA	GGAAGATCAG	AGGCAAGGAG	5640
CAGAACCTAG	AAAAAACTTT	GTCAAGCCTA	ATGAAACCAA	AACTTACTTT	TGGAAAGTGC	5700
AACATCATAT	GGCACCCTACT	AAAGATGAGT	TTGACTGCAA	AGCCTGGGCT	TATTTCTCTG	5760
ATGTTGACCT	GGAAAAAGAT	GTGCACTCAG	GCCTGATTGG	ACCCCTTCTG	GTCTGCCACA	5820
CTAACACACT	GAACCCTGCT	CATGGGAGAC	AAGTGACAGT	ACAGGAATTT	GCTCTGTTTT	5880
TCACCATCTT	TGATGAGACC	AAAAGCTGGT	ACTTCACTGA	AAATATGGAA	AGAAACTGCA	5940
GGGCTCCCTG	CAATATCCAG	ATGGAAGATC	CCACTTTTAA	AGAGAATTAT	CGCTTCCATG	6000
CAATCAATGG	CTACATAATG	GATACACTAC	CTGGCTTAGT	AATGGCTCAG	GATCAAAGGA	6060
TTGATGGTA	TCTGCTCAGC	ATGGGCAGCA	ATGAAAACAT	CCATTCTATT	CATTTTCAGTG	6120
GACATGTGTT	CACTGTACGA	AAAAAAGAGG	AGTATAAAAT	GGCACTGTAC	AATCTCTATC	6180
CAGGTGTTTT	TGAGACAGTG	GAAATGTTAC	CATCCAAAGC	TGGAATTTGG	CGGGTGGAAT	6240
GCCTTATTGG	CGAGCATCTA	CATGCTGGGA	TGAGCACACT	TTTTCTGGTG	TACAGCAATA	6300
AGTGTGAGAC	TCCCCTGGGA	ATGGCTTCTG	GACACATTAG	AGATTTTCAG	ATTACAGCTT	6360
CAGGACAATA	TGGACAGTGG	GCCCCAAAGC	TGGCCAGACT	TCATTATTCC	GGATCAATCA	6420
ATGCCTGGAG	CACCAAGGAG	CCCTTTTCTT	GGATCAAGGT	GGATCTGTTG	GCACCAATGA	6480
TTATTCACGG	CATCAAGACC	CAGGGTGCCC	GTCAGAAGTT	CTCCAGCCTC	TACATCTCTC	6540
AGTTTATCAT	CATGTATAGT	CTTGATGGGA	AGAAGTGGCA	GACTTATCGA	GGAAATTCCA	6600
CTGGAACCTT	AATGGTCTTC	TTTGGCAATG	TGGATTCAATC	TGGGATAAAA	CACAATATTT	6660
TTAACCCCTCC	AATTATTGCT	CGATACATCC	GTTTGCACCC	AACTCATTAT	AGCATTGCGA	6720
GCACTCTTCG	CATGGAGTTG	ATGGGCTGTG	ATTTAAATAG	TTGCAGCATG	CCATTGGGAA	6780
TGGAGAGTAA	AGCAATATCA	GATGCACAGA	TTACTGCTTC	ATCCTACTTT	ACCAATATGT	6840
TTGCCACCTG	GTCTCCTTCA	AAAGCTCGAC	TTACCTCCA	AGGGAGGAGT	AATGCCTGGA	6900
GACCTCAGGT	GAATAATCCA	AAAGAGTGGC	TGCAAGTGGG	CTTCCAGAAG	ACAATGAAAG	6960
TCACAGGAGT	AACTACTCAG	GGAGTAAAT	CTCTGCTTAC	CAGCATGTAT	GTGAAGGAGT	7020
TCCTCATCTC	CAGCAGTCAA	GATGGCCATC	AGTGGACTCT	CTTTTTTCAG	AATGGCAAAG	7080
TAAAGGTTTT	TCAGGGAAAT	CAAGACTCCT	TCACACCTGT	GGTGAACTCT	CTAGACCCAC	7140
CGTTACTGAC	TCGCTACCTT	CGAATTCACC	CCCAGAGTTG	GGTGCACCAG	ATTGCCCTGA	7200
GGATGGAGGT	TCTGGGCTGC	GAGGCACAGG	ACCTCTACTG	AGGGTGGCCA	CTGCAGCACC	7260
TGCCACTGCC	GTCACCTCTC	CCTCCTCAGC	TCCAGGGCAG	TGTCCCTCCC	TGGCTTGCCT	7320
TCTACCTTTG	TGCTAAATCC	TAGCAGACAC	TGCCTTGAAG	CCTCCTGAAT	TAACATATCAT	7380
CAGTCCTGCA	TTTCTTTGGT	GGGGGGCCAG	GAGGGTGCAT	CCAATTTAAC	TTAACTCTTA	7440
CCTATTTTCT	GCAGCTGCTC	CCAGATTACT	CCTTCCTTCC	AATATAACTA	GGCAAAAAGA	7500
AGTGAGGAGA	AACCTGCATG	AAAGCATTCT	TCCCTGAAAA	GTTAGGCCTC	TCAGAGTCAC	7560
CACTTCCTCT	GTTGTAGAAA	AACTATGTGA	TGAAACTTTG	AAAAAGATAT	TTATGATGTT	7620
AACATTTTCAG	GTTAAGCCTC	ATACGTTTAA	AATAAAACTC	TCAGTTGTTT	ATTATCCTGA	7680
TCAAGCATGG	AACAAAGCAT	GTTTCAGGAT	CAGATCAATA	CAATCTTGGA	GTCAAAAGGC	7740
AAATCATTTG	GACAATCTGC	AAAATGGAGA	GAATACAATA	ACTACTACAG	TAAAGTCTGT	7800
TTCTGCTTCC	TTACACATAG	ATATAATTAT	GTTATTTAGT	CATTATGAGG	GGCACATTCT	7860
TATCTCCAAA	ACTAGCATTG	TTAAACTGAG	AATTATAGAT	GGGGTTCAAG	AATCCCTAAG	7920
TCCCCTGAAA	TTATATAAGG	CATTCTGTAT	AAATGCAAAAT	GTGCATTTTT	CTGACGAGTG	7980
TCCATAGATA	TAAAGCCATT	TGGTCTTAAT	TCTGACCAAT	AAAAAAATAA	GTCAGGAGGA	8040
TGCAATTGTT	GAAAGCTTTG	AAATAAAATA	ACAATGTCTT	CTTGAAATTT	GTGATGGCCA	8100
AGAAAGAAAA	TGATGATGAC	ATTAGGCTTC	TAAAGGACAT	ACATTTAATA	TTTCTGTGGA	8160
AATATGAGGA	AAATCCATGG	TTATCTGAGA	TAGGAGATAC	AACTTTTGTA	ATTCTAATAA	8220
TGCACTCAGT	TTACTCTCTC	CCTCTACTAA	TTTCTGCTG	AAAATAACAC	AACAAAAATG	8280
TAACAGGGGA	AATTATATAC	CGTGACTGAA	AACTAGAGTC	CTACTTACAT	AGTTGAAATA	8340
TCAAGGAGGT	CAGAAGAAAA	TTGGACTGGT	GAAAACAGAA	AAAACACTCC	AGTCTGCCAT	8400
ATCACCACAC	AATAGGATCC	CCCTTCTTGC	CCTCCACCCC	CATAAGATTG	TGAAGGGTTT	8460
ACTGCTCCTT	CCATCTGCCT	GACCCCTTCA	CTATGACTAC	ACAGAATCTC	CTGATAGTAA	8520
AGGGGGCTGG	AGGCAAGGAT	AAGTTATAGA	GCAGTTGGAG	GAAGCATCCA	AAGATTGCAA	8580
CCCAGGGCAA	ATGGAAAACA	GGAGATCCTA	ATATGAAAGA	AAAATGGATC	CCAATCTGAG	8640
AAAAGGCAAA	AGAATGGCTA	CTTTTTTCTA	TGCTGGAGTA	TTTTCTAATA	ATCCTGCTTG	8700
ACCCTTATCT	GACCTCTTTG	GAAACTATAA	CATAGCTGTC	ACAGTATAGT	CACAATCCAC	8760

AAATGATGCA GGTGCAAATG GTTTATAGCC CTGTGAAGTT CTTAAAGTTT AGAGGCTAAC	8820
TTACAGAAAT GAATAAGTTG TTTTGTTTTA TAGCCCGGTA GAGGAGTTAA CCCCAAAGGT	8830
GATATGGTTT TATTTCTGT TATGTTTAACT TTAATAATCT TATTTTGGCA TTCTTTTCCC	8940
ATTGACTATA TACATCTCTA TTTCTCAAAT GTTCATGGAA CTAGCTCTTT TATTTTCTGT	9000
CTGGTTTCTT CAGTAATGAG TTAAATAAAA CATTGACACA TACAAAAAAA AAAAAAAAAA	9060
AAAAAAAAAA AAAAAAAAAA	9080

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2351 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: -linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met	Gln	Ile	Glu	Leu	Ser	Thr	Cys	Phe	Phe	Leu	Cys	Leu	Leu	Arg	Phe	1	5	10	15
Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser	20	25	30	
Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg	35	40	45	
Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val	50	55	60	
Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile	65	70	75	80
Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln	85	90	95	
Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser	100	105	110	
His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser	115	120	125	
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp	130	135	140	
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu	145	150	155	160
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	165	170	175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	180	185	190	
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	195	200	205	

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
 325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
 340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
 500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
 515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
 530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
 545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
 565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
 580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
 595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
 610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
 625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
 645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
 660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
 675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
 690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
 705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
 725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
 740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Pro
 755 760 765

Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp
 770 775 780

Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
 785 790 795 800
 Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
 805 810 815
 Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
 820 825 830
 Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
 835 840 845
 Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
 850 855 860
 Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
 865 870 875 880
 Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
 885 890 895
 Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
 900 905 910
 Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
 915 920 925
 Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
 930 935 940
 Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
 945 950 955 960
 Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
 965 970 975
 Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
 980 985 990
 Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
 995 1000 1005
 Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser Asn
 1010 1015 1020
 Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser Leu Leu
 1025 1030 1035 1040
 Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser Asp Thr
 1045 1050 1055
 Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
 1060 1065 1070

Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr
 1075 1080 1085
 Ser Ser Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile
 1090 1095 1100
 Pro Pro Asp Ala Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe
 1105 1110 1115 1120
 Leu Pro Glu Ser Ala Arg Trp Ile Gln Arg Thr His Gly Lys Asn Ser
 1125 1130 1135
 Leu Asn Ser Gly Gln Gly Pro Ser Pro Lys Gln Leu Val Ser Leu Gly
 1140 1145 1150
 Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys
 1155 1160 1165
 Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu
 1170 1175 1180
 Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn
 1185 1190 1195 1200
 Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu
 1205 1210 1215
 Ile Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln
 1220 1225 1230
 Ile His Thr Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu
 1235 1240 1245
 Leu Ser Thr Arg Gln Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala
 1250 1255 1260
 Pro Val Leu Gln Asp Phe Arg Ser Leu Asn Asp Ser Thr Asn Arg Thr
 1265 1270 1275 1280
 Lys Lys His Thr Ala His Phe Ser Lys Lys Gly Glu Glu Glu Asn Leu
 1285 1290 1295
 Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val Glu Lys Tyr Ala Cys
 1300 1305 1310
 Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe Val Thr Gln
 1315 1320 1325
 Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu Thr
 1330 1335 1340
 Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser
 1345 1350 1355 1360

Lys Asn Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr
 1365 1370 1375
 Asn Glu Lys Glu Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys
 1380 1385 1390
 Leu Thr Arg Ser His Ser Ile Pro Gln Ala Asn Arg Ser Pro Leu Pro
 1395 1400 1405
 Ile Ala Lys Val Ser Ser Phe Pro Ser Ile Arg Pro Ile Tyr Leu Thr
 1410 1415 1420
 Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro Ala Ala Ser Tyr
 1425 1430 1435 1440
 Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly
 1445 1450 1455
 Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
 1460 1465 1470
 Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser
 1475 1480 1485
 Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu
 1490 1495 1500
 Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr
 1505 1510 1515 1520
 Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser Pro Gly His
 1525 1530 1535
 Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr Glu Gly Ala Ile
 1540 1545 1550
 Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val Pro Phe Leu Arg Val
 1555 1560 1565
 Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu Leu Asp Pro Leu
 1570 1575 1580
 Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu Trp Lys
 1585 1590 1595 1600
 Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr
 1605 1610 1615
 Ile Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile
 1620 1625 1630
 Asn Glu Gly Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln
 1635 1640 1645

Gly Arg Thr Glu Arg Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg
 1650 1655 1660

His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu
 1665 1670 1675 1680

Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe
 1685 1690 1695

Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys
 1700 1705 1710

Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr
 1715 1720 1725

Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly
 1730 1735 1740

Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly
 1745 1750 1755 1760

Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly
 1765 1770 1775

Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val
 1780 1785 1790

Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu
 1795 1800 1805

Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn
 1810 1815 1820

Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His
 1825 1830 1835 1840

His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 1845 1850 1855

Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly
 1860 1865 1870

Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg
 1875 1880 1885

Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu
 1890 1895 1900

Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala
 1905 1910 1915 1920

Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg
 1925 1930 1935

Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val		
1940	1945	1950
Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser		
1955	1960	1965
Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val		
1970	1975	1980
Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly		
1985	1990	1995 2000
Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg		
2005	2010	2015
Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu		
2020	2025	2030
Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser		
2035	2040	2045
Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln		
2050	2055	2060
Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala		
2065	2070	2075 2080
Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala		
2085	2090	2095
Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe		
2100	2105	2110
Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly		
2115	2120	2125
Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val		
2130	2135	2140
Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn		
2145	2150	2155 2160
Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser		
2165	2170	2175
Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser		
2180	2185	2190
Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln		
2195	2200	2205
Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro		
2210	2215	2220

Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro
 2225 2230 2235 2240
 Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr
 2245 2250 2255
 Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu Leu Thr
 2260 2265 2270
 Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His
 2275 2280 2285
 Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly
 2290 2295 2300
 Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
 2305 2310 2315 2320
 Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile
 2325 2330 2335
 Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
 2340 2345 2350

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4832 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CTCGAGCTAA AGATATTTTA GAGAAGAATT AACCTTTTGC TTCTCCAGTT GAACATTTGT	60
AGCAATAAGT CATGCAAATA GAGCTCTCCA CCTGCTTCTT TCTGTGCCTT TTGCGATTCT	120
GCTTTAGTGC CACCAGAAGA TACTACCTGG GTGCAGTGGG ACTGTCATGG GACTATATGC	180
AAAGTGATCT CGGTGAGCTG CCTGTGGACG CAAGATTTCC TCCTAGAGTG CCAAATCTT	240
TTCCATTCAA CACCTCAGTC GTGTACAAA AGACTCTGTT TGTAGAATTC ACGGATCACC	300
TTTTCAACAT CGCTAAGCCA AGGCCACCTT GGATGGGTCT GCTAGGTCCT ACCATCCAGG	360
CTGAGGTTTA TGATACAGTG GTCATTACAC TTAAGAACAT GGCTTCCCAT CCTGTCAGTC	420
TTTATGCTGT TGGTGTATCC TACTGGAAAG CTTCTGAGGG AGCTGAATAT GATGATCAGA	480
CCAGTCAAAG GGAGAAAGAA GATGATAAAG TCTTCCCTGG TGGAAGCCAT ACATATGTCT	540
GGCAGGTCCT GAAAGAGAAT GGTCCAATGG CCTCTGACCC ACTGTGCCTT ACCTACTCAT	600
ATCTTTCTCA TGTGGACCTG GTAAAAGACT TGAATTCAGG CCTCATTGGA GCCCTACTAG	660
TATGTAGAGA AGGGAGTCTG GCCAAGGAAA AGACACAGAC CTTGCACAAA TTTATACTAC	720
TTTTTGCTGT ATTTGATGAA GGGAAAAGTT GGCACCTCAG AACAAAGAAC TCCTTGATGC	780
AGGATAGGGA TGCTGCATCT GCTCGGGCCT GGCCTAAAT GCACACAGTC AATGGTTATG	840
TAAACAGGTC TCTGCCAGGT CTGATTGGAT GCCACAGGAA ATCAGTCTAT TGGCATGTGA	900
TTGGAATGGG CACCACTCCT GAAGTGCACCT CAATATTCCT CGAAGGTCAC ACATTTCTTG	960
TGAGGAACCA TCGCCAGGCG TCCTTGGAAT TCTCGCCAAT AACTTTCTCT ACTGCTCAAA	1020
CACTCTTGAT GGACCTTGGA CAGTTTCTAC TGTTTTGTC TATCTCTTCC CACCAACATG	1080
ATGGCATGGA AGCTTATGTC AAAGTAGACA GCTGTCCAGA GGAACCCCAA CTACGAATGA	1140
AAAATAATGA AGAAGCGGAA GACTATGATG ATGATCTTAC TGATTCTGAA ATGGATGTGG	1200
TCAGGTTTGA TGATGACAAC TCTCCTTCCT TTATCCAAAT TCGCTCAGTT GCCAAGAAGC	1260

ATCCTAAAAC	TTGGGTACAT	TACATTGCTG	CTGAAGAGGA	GGACTGGGAC	TATGCTCCCT	1320
TAGTCCTCGC	CCCCGATGAC	AGAAGTTATA	AAAGTCAATA	TTTGAACAAT	GGCCCTCAGC	1380
GGATTGGTAG	GAAGTACAAA	AAAGTCCGAT	TTATGGCATA	CACAGATGAA	ACCTTTAAGA	1440
CTCGTGAAGC	TATTCAGCAT	GAATCAGGAA	TCTTGGGACC	TTTACTTTAT	GGGGAAGTTG	1500
GAGACACACT	GTTGATTATA	TTTAAGAATC	AAGCAAGCAG	ACCATATAAC	ATCTACCCTC	1560
ACGGAATCAC	TGATGTCCGT	CCTTTGTATT	CAAGGAGATT	ACCAAAAGGT	GTAAAACATT	1620
TGAAGGATTT	TCCAATTCTG	CCAGGAGAAA	TATTCAAATA	TAAATGGACA	GTGACTGTAG	1680
AAGATGGGCC	AACTAAATCA	GATCCTCGGT	GCCTGACCCG	CTATTACTCT	AGTTTCGTTA	1740
ATATGGAGAG	AGATCTAGCT	TCAGGACTCA	TTGGCCCTCT	CCTCATCTGC	TACAAAGAAT	1800
CTGTAGATCA	AAGAGGAAAC	CAGATAATGT	CAGACAAGAG	GAATGTCATC	CTGTTTTCTG	1860
TATTTGATGA	GAACCGAAGC	TGGTACCTCA	CAGAGAATAT	ACAACGCTTT	CTCCCCAATC	1920
CAGCTGGAGT	GCAGCTTGAG	GATCCAGAGT	TCCAAGCCTC	CAACATCATG	CACAGCATCA	1980
ATGGCTATGT	TTTTGATAGT	TGCGAGTTGT	CAGTTTGTIT	GCATGAGGTG	GCATACTGGT	2040
ACATTCTAAG	CATTGGAGCA	CAGACTGACT	TCCTTTCTGT	CTTCTTCTCT	GGATATACCT	2100
TCAAACACAA	AATGGTCTAT	GAAGACACAC	TCACCCTATT	CCCATTCTCA	GGAGAAACTG	2160
TCTTCATGTC	GATGGAAAAC	CCAGGTCTAT	GGATTCTGGG	GTGCCACAAC	TCAGACTTTC	2220
GGAACAGAGG	CATGACCGCC	TTACTGAAGG	TTTCTAGTTG	TGACAAGAAC	ACTGGTGATT	2280
ATTACGAGGA	CAGTTATGAA	GATATTTTCAG	CATACTTGCT	GAGTAAAAAC	AATGCCATTG	2340
AACCAAGAAG	CTTCTCCAG	AACCCACCAG	TCTTGAAACG	CCATCAACGG	GAAATAACTC	2400
GTACTACTCT	TCAGTCAGAT	CAAGAGGAAA	TTGACTATGA	TGATACCATA	TCAGTTGAAA	2460
TGAAGAAGGA	AGATTTTGAC	ATTTATGATG	AGGATGAAAA	TCAGAGCCCC	CGCAGCTTTC	2520
AAAAGAAAAC	ACGACACTAT	TTTATTGCTG	CAGTGGAGAG	GCTCTGGGAT	TATGGGATGA	2580
GTAGCTCCCC	ACATGTTCTA	AGAAACAGGG	CTCAGAGTGG	CAGTGTCCCT	CAGTTCAAGA	2640
AAGTTGTTTT	CCAGGAATTT	ACTGATGGCT	CCTTTACTCA	GCCCTTATAC	CGTGGAGAAC	2700
TAAATGAACA	TTTGGGACTC	CTGGGGCCAT	ATATAAGAGC	AGAAGTTGAA	GATAATATCA	2760
TGGTAACTTT	CAGAAATCAG	GCCTCTCGTC	CCTATTCCCT	CTATTCTAGC	CTTATTTCTT	2820
ATGAGGAAGA	TCAGAGGCAA	GGAGCAGAAC	CTAGAAAAAA	CTTTGTCAAG	CCTAATGAAA	2880
CCAAAACCTA	CTTTTGGAAG	GTGCAACATC	ATATGGCACC	CACTAAAGAT	GAGTTTGACT	2940
GCAAAGCCTG	GGCTTATTTT	TCTGATGTTG	ACCTGGAAAA	AGATGTGCAC	TCAGGCCTGA	3000
TTGGACCCCT	TCTGGTCTGC	CACACTAACA	CACTGAACCC	TGCTCATGGG	AGACAAGTGA	3060
CAGTACAGGA	ATTGCTCTG	TTTTTCACCA	TCTTTGATGA	GACCAAAAGC	TGGTACTTCA	3120
CTGAAAATAT	GGAAAGAAAC	TGCAGGGCTC	CCTGCAATAT	CCAGATGGAA	GATCCCACTT	3180
TTAAAGAGAA	TTATCGCTTC	CATGCAATCA	ATGGCTACAT	AATGGATACA	CTACCTGGCT	3240
TAGTAATGGC	TCAGGATCAA	AGGATTGAT	GGTATCTGCT	CAGCATGGGC	AGCAATGAAA	3300
ACATCCATT	TATTCATTT	AGTGGACATG	TGTTCACTGT	ACGAAAAAAA	GAGGAGTATA	3360
AAATGGCACT	GTACAATCTC	TATCCAGGTG	TTTTTGAGAC	AGTGGAAATG	TTACCATCCA	3420
AAGCTGGAAT	TTGGCGGGTG	GAATGCCTTA	TTGGCGAGCA	TCTACATGCT	GGGATGAGCA	3480
CACTTTTTCT	GGTGTACAGC	AATAAGTGTC	AGACTCCCTT	GGGAATGGCT	TCTGGACACA	3540
TTAGAGATTT	TCAGATTACA	GCTTCAGGAC	AATATGGACA	GTGGGCCCCA	AAGCTGGCCA	3600
GACTTCATTA	TTCCGGATCA	ATCAATGCCT	GGAGCACCAA	GGAGCCCTTT	TCTTGGATCA	3660
AGGTGGATCT	GTTGGCACCA	ATGATTATTC	ACGGCATCAA	GACCCAGGGT	GCCCGTCAGA	3720
AGTTCTCCAG	CCTCTACATC	TCTCAGTTTA	TCATCATGTA	TAGTCTTGAT	GGGAAGAAGT	3780
GGCAGACTTA	TCGAGGAAAT	TCCACTGGAA	CCTTAATGGT	CTTCTTTGGC	AATGTGGATT	3840
CATCTGGGAT	AAAACACAAT	ATTTTTAACC	CTCCAATTAT	TGCTCGATAC	ATCCGTTTGC	3900
ACCCAACCTA	TTATAGCATT	CGCAGCACTC	TTGCGATGGA	GTTGATGGGC	TGTGATTTAA	3960
ATAGTTGCAG	CATGCCATTG	GGAATGGAGA	GTAAAGCAAT	ATCAGATGCA	CAGATTACTG	4020
CTTCATCCTA	CTTTACCAAT	ATGTTTGCCA	CCTGGTCTCC	TTCAAAAGCT	CGACTTCACC	4080
TCCAAGGGAG	GAGTAATGCC	TGGAGACCTC	AGGTGAATAA	TCCAAGAGAG	TGGCTGCAAG	4140
TGGACTTCCA	GAAGACAATG	AAAGTCACAG	GAGTAACTAC	TCAGGGAGTA	AAATCTCTGC	4200
TTACCAGCAT	GTATGTGAAG	GAGTTCCTCA	TCTCCAGCAG	TCAAGATGGC	CATCAGTGGG	4260
CTCTCTTTTT	TCAGAATGGC	AAAGTAAAGG	TTTTTCAGGG	AAATCAAGAC	TCCTTCACAC	4320
CTGTGGTGAA	CTCTCTAGAC	CCACCGTTAC	TGACTCGCTA	CCTTCGAATT	CACCCCCAGA	4380
GTTGGGTGCA	CCAGATTGCC	CTGAGGATGG	AGGTCTGGG	CTGCGAGGCA	CAGGACCTCT	4440
ACTGAGGGTG	GCCACTGCAG	CACCTGCCAC	TGCCGTCAAC	TCTCCCTCCT	CAGCTCCAGG	4500

GCAGTGTCCC	TCCCTGGCTT	GCCTTCTACC	TTTGTGCTAA	ATCCTAGCAG	ACACTGCCTT	4560
GAAGCCTCCT	GAATTAACCTA	TCATCAGTCC	TGCATTTCTT	TGGTGGGGGG	CCAGGAGGGT	4620
GCATCCAATT	TAACTTAACT	CTTACCTATT	TTCTGCAGCT	GCTCCCAGAT	TACTCCTTCC	4680
TTCCAATATA	ACTAGGCAAA	AAGAAGTGAG	GAGAAACCTG	CATGAAAGCA	TTCTTCCCTG	4740
AAAAGTTAGG	CCTCTCAGAG	TCACCACTTC	CTCTGTTGTA	GAAAACTAT	GTGATGAAAC	4800
TTTGAAAAAG	ATATTATGA	TGTTGCGGCC	GC			4832

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1457 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: -linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Gln	Ile	Glu	Leu	Ser	Thr	Cys	Phe	Phe	Leu	Cys	Leu	Leu	Arg	Phe	1	5	10	15
Cys	Phe	Ser	Ala	Thr	Arg	Arg	Tyr	Tyr	Leu	Gly	Ala	Val	Glu	Leu	Ser	20	25	30	
Trp	Asp	Tyr	Met	Gln	Ser	Asp	Leu	Gly	Glu	Leu	Pro	Val	Asp	Ala	Arg	35	40	45	
Phe	Pro	Pro	Arg	Val	Pro	Lys	Ser	Phe	Pro	Phe	Asn	Thr	Ser	Val	Val	50	55	60	
Tyr	Lys	Lys	Thr	Leu	Phe	Val	Glu	Phe	Thr	Asp	His	Leu	Phe	Asn	Ile	65	70	75	80
Ala	Lys	Pro	Arg	Pro	Pro	Trp	Met	Gly	Leu	Leu	Gly	Pro	Thr	Ile	Gln	85	90	95	
Ala	Glu	Val	Tyr	Asp	Thr	Val	Val	Ile	Thr	Leu	Lys	Asn	Met	Ala	Ser	100	105	110	
His	Pro	Val	Ser	Leu	His	Ala	Val	Gly	Val	Ser	Tyr	Trp	Lys	Ala	Ser	115	120	125	
Glu	Gly	Ala	Glu	Tyr	Asp	Asp	Gln	Thr	Ser	Gln	Arg	Glu	Lys	Glu	Asp	130	135	140	
Asp	Lys	Val	Phe	Pro	Gly	Gly	Ser	His	Thr	Tyr	Val	Trp	Gln	Val	Leu	145	150	155	160
Lys	Glu	Asn	Gly	Pro	Met	Ala	Ser	Asp	Pro	Leu	Cys	Leu	Thr	Tyr	Ser	165	170	175	
Tyr	Leu	Ser	His	Val	Asp	Leu	Val	Lys	Asp	Leu	Asn	Ser	Gly	Leu	Ile	180	185	190	
Gly	Ala	Leu	Leu	Val	Cys	Arg	Glu	Gly	Ser	Leu	Ala	Lys	Glu	Lys	Thr	195	200	205	

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220
 Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240
 Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255
 Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270
 Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285
 Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300
 Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320
 Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
 325 330 335
 Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
 340 345 350
 Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365
 Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 370 375 380
 Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400
 Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415
 Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 420 425 430
 Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 435 440 445
 Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460
 Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480
 Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
 500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
 515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
 530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg
 545 550 555 560

Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu
 565 570 575

Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val
 580 585 590

Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu
 595 600 605

Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp
 610 615 620

Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
 625 630 635 640

Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp
 645 650 655

Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe
 660 665 670

Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr
 675 680 685

Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro
 690 695 700

Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly
 705 710 715 720

Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp
 725 730 735

Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys
 740 745 750

Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu
 755 760 765

Lys Arg His Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln
 770 775 780

Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu
 785 790 795 800
 Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe
 805 810 815
 Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp
 820 825 830
 Asp Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln
 835 840 845
 Ser Gly Ser Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr
 850 855 860
 Asp Gly Ser Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His
 865 870 875 880
 Leu Gly Leu Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile
 885 890 895
 Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser
 900 905 910
 Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg
 915 920 925
 Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 930 935 940
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp
 945 950 955 960
 Ala Tyr Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu
 965 970 975
 Ile Gly Pro Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His
 980 985 990
 Gly Arg Gln Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe
 995 1000 1005
 Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys
 1010 1015 1020
 Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn
 1025 1030 1035 1040
 Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly
 1045 1050 1055
 Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met
 1060 1065 1070

Gly Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe
 1075 1080 1085
 Thr Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr
 1090 1095 1100
 Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile
 1105 1110 1115 1120
 Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser
 1125 1130 1135
 Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met
 1140 1145 1150
 Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr
 1155 1160 1165
 Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile
 1170 1175 1180
 Asn Ala Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu
 1185 1190 1195 1200
 Leu Ala Pro Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln
 1205 1210 1215
 Lys Phe Ser Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu
 1220 1225 1230
 Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu
 1235 1240 1245
 Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile
 1250 1255 1260
 Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His
 1265 1270 1275 1280
 Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu
 1285 1290 1295
 Asn Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp
 1300 1305 1310
 Ala Gln Ile Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp
 1315 1320 1325
 Ser Pro Ser Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp
 1330 1335 1340
 Arg Pro Gln Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln
 1345 1350 1355 1360

Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln Gly Val Lys Ser Leu
 1365 1370 1375
 Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp
 1380 1385 1390
 Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
 1395 1400 1405
 Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro
 1410 1415 1420
 Pro Leu Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His
 1425 1430 1435 1440
 Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu
 1445 1450 1455

Tyr

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
 1 5 10 15
 Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu
 20 25 30
 Ser Lys Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg
 35 40 45
 His Pro Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Pro Pro Thr Pro
 50 55 60
 Pro Thr Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg Thr
 65 70 75 80
 Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser
 85 90 95
 Val Glu Met Lys
 100

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGAGGCATGA	CCGCCTTACT	GAAGGTTTCT	AGTTGTGACA	AGAACACTGG	TGATTATTAC	60
GAGGACAGTT	ATGAAGATAT	TTCAGCATAC	TTGCTGAGTA	AAAACAATGC	CATTGAACCA	120
AGAAGCTTCT	CCCAGAATTC	TAGACACCCT	AGCACTAGGC	AAAAGCAATT	TAATGCCACC	180
CCTCCTACAC	CACCAACCCC	ACCAGTACTG	AAACGCCATC	AACGGGAAAT	AACTCGTACT	240
ACTCTTCAGT	CTGATCAAGA	GGAAATTGAC	TATGATGATA	CCATATCAGT	TGAAATGAAG	300

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Arg His Pro Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Pro Pro
1. 5 10 15

Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
20 25

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi). SEQUENCE DESCRIPTION: SEQ ID NO:51:

TCGCGACACC CTAGCACTAG GCAAAAGCAA TTTAATGCCA CCCCACCAGT CCTGAAACGC 60
CATCAACGGG AAATAACGCG T 81

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACTACTCTTC AATCTGATCA AGAGGAA

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
CGCGCCGCTC GAGTCTACAA TGGCTTTGCC TTTTGCTTTA CTG 43

(2) INFORMATION FOR SEQ ID NO:54:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: -linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
GCGCCCATCG ATTTATTCCT TCCTCCTTAA CCTTTCTTGC AAG 43

(2) INFORMATION FOR SEQ ID NO:55:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
CGCGCCGCTC GAGCATCCCA ATGGCCCTGT CCTTTTCTTT ACTGATGG 48

(2) INFORMATION FOR SEQ ID NO:56:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:
CCATCGATTG AATCCTTCCT CCTTAATCTT TTTTGCAAG 39

(2) INFORMATION FOR SEQ ID NO:57:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:
CCGGATCCTC TACAATGGCT TTGCCTTTTG CTTTACTG 38

(2) INFORMATION FOR SEQ ID NO:58:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
CGCGCCGGCG GCCGCTTATT CCTTCCTCCT TAACCTTTCT TGCAAG

46

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:
CCGGATCCCA TCCCAATGGC CCGTCCTTT TCTTACTGA TGG

43

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
CGCGCCGGCG GCCGCTCAAT CCTTCCTCCT TAATCTTTT TGCAAG

46

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
AGCTTGCTGT TTGTGTGCTG CCTCTGAAGT CCACACTGAA CAAACTTCAG CCTACTCATG
TCCCTAAAAT GGGCAAACAT TGCAAGCAGC

60
90

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:
AAACAGCAAA CACACAGCCC TCCCTGCCTG CTGACCTTGG AGCTGGGGCA GAGGTCAGAG
ACCTCTCTGA

60
70

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

AGCTTCAGAG AGGTCTCTGA CCTCTGCCCC AGCTCCAAGG TCAGCAGGCA GGGAGGGCTG
TGTGTTTGCT GTTTGCTGCT TG

60
82

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CAATGTTTGC CCATTITAGG GACATGAGTA GGCTGAAGTT TGTTTCAGTGT GGACTTCAGA
GGCAGCACAC AAACAGCA

60
78

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

AATTCGCTGT TTGTGTGCTG CCTCTGAAGT CCACACTGAA CAAACTTCAG CCTACTCATG
TCCCTAAAT GGGCAAACAT TGCAAGCAGC

60
90

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAACAGCAAA CACACAGCCC TCCCTGCCTG CTGACCTTGG AGCTGGGGCA GAGGTCAGAG
ACCTCTCTGG

60
70

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

AATTCAGAG AGGTCTCTGA CCTCTGCCCC AGCTCCAAGG TCAGCAGGCA GGGAGGGCTG
TGTGTTTGCT GTTTGCTGCT TG

60
82

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:
CAATGTTTGC CCATTTTAGG GACATGAGTA GGCTGAAGTT TGTTCAGTGT GGACTTCAGA
GGCAGCACAC AAACAGCG 60
78

(2) INFORMATION FOR SEQ ID NO:69:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:
CGCGCCGCCC GGGGTAGATC TTGCTACCAG TGG 33

(2) INFORMATION FOR SEQ ID NO:70:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:
GCGCCCGCGG CCGCCACTGT CCCAGGTCAG TGGTGGTGCC 40

(2) INFORMATION FOR SEQ ID NO:71:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:
CGCGCCGGCG GCCGCTCTAC AATGGCCTTG ACCTTTGCTT TACTGG 46

(2) INFORMATION FOR SEQ ID NO:72:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:
GCGCCCATCG ATTCATTCTT TACTTCTTAA ACTTTCTTGC AAG 43

(2) INFORMATION FOR SEQ ID NO:73:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:
CGCGCCGGCG GCCGCTCTAC AATGGCCTTG ACCTTTGCTT TACTGG 46

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCGCCCATCG ATTCATTCCT TACTTCTTAA ACTTTCTTGC AAG

43

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Asn Ser Arg His Pro Ser

1

5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr

1

5

10

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

AATTCGCGAC ACCCTAGC

18

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAAAACCCAC CAGTCTTGAA ACGCCATCAA CGGGAAATAA CG

42

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
GCGCTGTGGG ATCGGTTTTG GGTGGTCAGA AC

32

(2) INFORMATION FOR SEQ ID NO:80:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:
TTTGCGGTAG TTGCCCTTA TTGC

24

(2) INFORMATION FOR SEQ ID NO:81:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
 Arg Thr Leu Gln Ser Asp
 1 5

(2) INFORMATION FOR SEQ ID NO:82:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
CGTACTCTTC AGTCT

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(2) INFORMATION FOR SEQ ID NO:83:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
GCATGAGAAG TCAGACTAG

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(2) INFORMATION FOR SEQ ID NO:84:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
TGCATGCCTG CAGGTC